

SEQUENCE LISTING

<110> Bayer Aktiengesellschaft

<120> Ligand binding domains of Ultraspiracle (USP) proteins

<130> Le A 34 772

<140>

<141>

<150> DE 100 36 461.6

<151> 2000-07-25

<160> 2

<170> PatentIn Ver. 2.1

<210> 1

<211> 262

<212> PRT

<213> Heliothis virescens

<400> 1

Val	Gln	Glu	Leu	Ser	Ile	Glu	Arg	Leu	Leu	Glu	Met	Glu	Ser	Leu	Val
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Ala	Asp	Pro	Ser	Glu	Glu	Phe	Gln	Phe	Leu	Arg	Val	Gly	Pro	Asp	Ser
			20					25					30		

Asn	Val	Pro	Pro	Lys	Phe	Arg	Ala	Pro	Val	Ser	Ser	Leu	Cys	Gln	Ile
	35						40					45			

Gly	Asn	Lys	Gln	Ile	Ala	Ala	Leu	Val	Val	Trp	Ala	Arg	Asp	Ile	Pro
50					55					60					

His	Phe	Ser	Gln	Leu	Glu	Met	Glu	Asp	Gln	Ile	Leu	Leu	Ile	Lys	Gly
65					70					75				80	

Ser	Trp	Asn	Glu	Leu	Leu	Leu	Phe	Ala	Ile	Ala	Trp	Arg	Ser	Met	Glu
			85						90					95	

Phe	Leu	Thr	Glu	Glu	Arg	Asp	Gly	Val	Asp	Gly	Thr	Gly	Asn	Arg	Thr
	100						105						110		

Thr	Ser	Pro	Pro	Gln	Leu	Met	Cys	Leu	Met	Pro	Gly	Met	Thr	Leu	His
	115						120					125			

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Arg Asn Ser Ala Leu Gln Ala Gly Val Gly Gln Ile Phe Asp Arg Val
130 135 140

Leu Ser Glu Leu Ser Leu Lys Met Arg Thr Leu Arg Val Asp Gln Ala
145 150 155 160

Glu Tyr Val Ala Leu Lys Ala Ile Ile Leu Leu Asn Pro Asp Val Lys
165 170 175

Gly Leu Lys Asn Arg Gln Glu Val Glu Val Leu Arg Glu Lys Met Phe
180 185 190

Leu Cys Leu Asp Glu Tyr Cys Arg Arg Ser Arg Ser Ser Glu Glu Gly
195 200 205

Arg Phe Ala Ala Leu Leu Leu Arg Leu Pro Ala Leu Arg Ser Ile Ser
210 215 220

Leu Lys Ser Phe Glu His Leu Phe Phe Phe His Leu Val Ala Asp Thr
225 230 235 240

Ser Ile Ala Gly Tyr Ile Arg Asp Ala Leu Arg Asn His Ala Pro Pro
245 250 255

Ile Asp Thr Asn Met Met
260

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<211> 466

<212> PRT

<213> *Heliothis virescens*

<400> 2

Met Ser Val Ala Lys Lys Asp Lys Pro Thr Met Ser Val Thr Ala Leu
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Ile Asn Trp Ala Arg Pro Leu Pro Pro Gly Gln Gln Gln Gln Pro Met
20 25 30

Thr Pro Thr Ser Pro Gly Asn Met Leu Gln Pro Met Ala Thr Pro Ser
35 40 45

Asn Leu Pro Thr Val Asp Cys Ser Leu Asp Ile Gln Trp Leu Asn Leu
50 55 60

Glu Gly Gly Phe Met Ser Pro Met Ser Pro Pro Glu Met Lys Pro Asp

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65	70	75	80
Thr Ala Met Leu Asp Gly Leu Arg Asp Asp Ser Thr Pro Pro Pro Ala			
85	90	95	
Phe Lys Asn Tyr Pro Pro Asn His Pro Leu Ser Gly Ser Lys His Leu			
100	105	110	
Cys Ser Ile Cys Gly Asp Arg Ala Ser Gly Lys His Tyr Gly Val Tyr			
115	120	125	
Ser Cys Glu Gly Cys Lys Gly Phe Phe Lys Arg Thr Val Arg Lys Asp			
130	135	140	
Leu Thr Tyr Ala Cys Arg Glu Glu Arg Asn Cys Ile Ile Asp Lys Arg			
145	150	155	160
Gln Arg Asn Arg Cys Gln Tyr Cys Arg Tyr Gln Lys Cys Leu Ala Cys			
165	170	175	
Gly Met Lys Arg Glu Ala Val Gln Glu Glu Arg Gln Arg Ala Ala Arg			
180	185	190	
Gly Thr Glu Asp Ala His Pro Ser Ser Ser Val Gln Val Gln Glu Leu			
195	200	205	
Ser Ile Glu Arg Leu Leu Glu Met Glu Ser Leu Val Ala Asp Pro Ser			
210	215	220	
Glu Glu Phe Gln Phe Leu Arg Val Gly Pro Asp Ser Asn Val Pro Pro			
225	230	235	240
Lys Phe Arg Ala Pro Val Ser Ser Leu Cys Gln Ile Gly Asn Lys Gln			
245	250	255	
Ile Ala Ala Leu Val Val Trp Ala Arg Asp Ile Pro His Phe Ser Gln			
260	265	270	
Leu Glu Met Glu Asp Gln Ile Leu Leu Ile Lys Gly Ser Trp Asn Glu			
275	280	285	
Leu Leu Leu Phe Ala Ile Ala Trp Arg Ser Met Glu Phe Leu Thr Glu			
290	295	300	
Glu Arg Asp Gly Val Asp Gly Thr Gly Asn Arg Thr Thr Ser Pro Pro			
305	310	315	320
Gln Leu Met Cys Leu Met Pro Gly Met Thr Leu His Arg Asn Ser Ala			

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325	330	335
Leu Gln Ala Gly Val Gly Gln Ile Phe Asp Arg Val Leu Ser Glu Leu		
340	345	350
Ser Leu Lys Met Arg Thr Leu Arg Val Asp Gln Ala Glu Tyr Val Ala		
355	360	365
Leu Lys Ala Ile Ile Leu Leu Asn Pro Asp Val Lys Gly Leu Lys Asn		
370	375	380
Arg Gln Glu Val Glu Val Leu Arg Glu Lys Met Phe Leu Cys Leu Asp		
385	390	395 400
Glu Tyr Cys Arg Arg Ser Arg Ser Ser Glu Glu Gly Arg Phe Ala Ala		
405	410	415
Leu Leu Leu Arg Leu Pro Ala Leu Arg Ser Ile Ser Leu Lys Ser Phe		
420	425	430
Glu His Leu Phe Phe Phe His Leu Val Ala Asp Thr Ser Ile Ala Gly		
435	440	445
Tyr Ile Arg Asp Ala Leu Arg Asn His Ala Pro Pro Ile Asp Thr Asn		
450	455	460
Met Met		
465		